Input file F1h14273new; Ouput File F1h14273tra
Sequence length 1743

```
TCCGGACTAGTTCTAGACCGGCTGCGGGGGCCGCCAGGGCCCGGGA

 M   S   P   E   C   A   R   A   A                                                  9
ATG TCC CCT GAA TGC GCG CGG GCA GCG                                                27

 G   D   A   P   L   R   S   L   E   Q   A   N   R   T   R   F   P   F   F   S      29
GGC GAC GCG CCC TTG CGC AGC CTG GAG CAA GCC AAC CGC ACC CGC TTT CCC TTC TTC TCC    87

 D   V   K   G   D   H   R   L   V   A   A   E   T   V   V   L   C   V   L   L      49
GAC GTC AAG GGC GAC CAC CGG CTG GTG GCG GCG GAG ACA GTG GTG CTC TGC GTG CTA CTC   147

 I   F   A   V   S   L   L   G   N   V   C   A   C   L   V   L   V   L   A   V      69
ATC TTT GCA GTG TCG CTG CTG GGC AAC GTG TGC GCC TGC CTC GTA CTC GTG CTG GCC GTG   207

 R   R   G   A   T   A   C   L   L   D   L   L   A   W   L   L   ...                89
CGC CGC GGC GCG ACT GCC TGC ...                                                   267

 S   A   I   P   L   V   L   A   V   R   W   T   E   A   W   L   L   G   P   V     109
AGC GCT ATC CCT CTG GTG CTG GCC GTG CGC TGG ACT GAG GCC TGG CTG CTG GGC CCC GTT   327

 A   C   H   L   F   L   Y   V   M   T   L   S   G   S   V   T   I   L   T   L     129
GCC TGC CAC CTG TTC CTC TAC GTG ATG ACC CTG AGC GGC AGC GTC ACC ATC CTC ACG CTG   387

 A   V   S   L   E   R   M   V   C   I   V   H   L   Q   R   G   V   R   G   G     149
GCC GTC AGC CTG GAG CGC ATG GTG TGC ATC GRG CAC CTG CAG CGC GGC GTG CGG GGG GGT   447

 P   G   R   A   R   A   A   L   I   W   G   Y   S   A   V   A                     169
CCT CGG CGG GCG CGG GCA GCG GCG CTC ATC TGG GCC TAT TCG GCC GTC GCC               507

 A   L   P   L   C   V   F   F   R   V   V   P   Q   R   L   P   G   A   D   Q     189
GCT CTG CCT CTC TGC GTC TTC TTT CGA GTC GTC CCG CAA CGG CTC CCC GGC GCC GAC CAG   567
```

TO FIG. 1B.

FIG. 1A.

FROM FIG. 1A.

```
 E   I   S   I   C   T   L   I   W   P   T   I   P   G   E   I   S   W   D   V   209
GAA ATT TCG ATT TGC ACA CTG ATT TGG CCC ACC ATT CCT GGA GAG ATC TCG TGG GAT GTC  627

 S   F   V   T   L   N   F   L   V   P   G   L   V   I   V   I   S   Y   S   K   229
TCT TTT GTT ACT TTG AAC TTC TTG GTG CCA GGA CTG GTC ATT GTG ATC AGT TAC TCC AAA  687

 I   L   Q   I   T   K   A   S   R   K   R   L   T   V   S   L   A   Y   S   E   249
ATT TTA CAG ATC ACA AAG GCA TCA AGG AAG CGC CTC ACC GTA AGC CTG GCC TAC TCG GAG  747

 S   H   Q   I   R   V   S   Q   Q   D   F   R   L   F   R   T   L   F   L   L   269
AGC CAC CAG ATC CGC GTG TCC CAG CAG GAC TTC CGC CTC TTC CGC ACC CTC TTC CTC CTC  807

 M   V   S   F   F   I   M   W   S   P   I   I   I   T   L   L   L   I   L   I   289
ATG GTC TCC TTC TTC ATC ATG TGG AGC CCC ATC ATC ATC ACC CTC CTC CTC ATC CTG ATC  867

 Q   N   F   K   Q   D   L   V   I   W   P   S   L   F   V   V   A   F   309
CAG AAC TTC AAG CAA GAC CTG GTC ATC TGG CCG TCC CTC TTC GTG GTG GCC TTC  927
```

TO FIG. 1C.

FIG. 1B.

FROM FIG. 1B.

```
 T   F   A   N   S   A   L   N   P   I   L   Y   N   M   T   L   C   R   N   E    329
ACA TTT GCT AAT TCA GCC CTA AAC CCC ATC CTC TAC AAC ATG ACA CTG TGC AGG AAT GAG  987

 W   K   I   F   C   F   W   F   P   E   K   G   A   I   L       T   D   T    349
TGG AAG AAA ATT TGC TGC TTC TGG TTC CCA GAA AAG GGA GCC ATT TTA ACA GAC ACA 1047

 S   V   K   R   N   D   L   S   I   I   S   G   .    362
TCT GTC AAA AGA AAT GAC TTG TCG ATT ATT TCT GGC TAA 1086
```

TTTTCTTTATAGCCGGAGTTCTCACACCTGGGCGAGCTGTGGCATGCTTTAAACAGAGTTCATTTCCAGTACCCTCCA

TCAGTGCACCCTGCTTTAAGAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAGGGGTGATCACCAA

GTTTCATAATATTTCCCTTTATAAAGGATTTGTTGGCCAGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGG

AGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGACCAACATGGTGAGACCCCGTCTCTACTA

AAAATAAAAAAAAAAAAAATTAGCTGGGAGTGGTGGCGCACCTGTAATCCCAGCTACTTGGGAGGCTGAACCAGGAGAAT

CTCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCATTGCACTCCAACCAGGCAACAAGAGTGAAAC

TCCATCTTAAAAAAAAAAAAAAAAAGATTTGTTATGGGTTCCTTTAAATGTGAACTTTTTAGTGTGTTGTAATATG

ATCAAATTAATAAATATTTATTTATGACTGTTCAGCAAAAAAAAAAAAAAAAAAAAGGGCGG

RTA01/2057957v1

FIG. 1C.

Sequence	Description	score	E-value	N
7tm_1	PF00001 7 transmembrane receptor (rhodopsin	119.9	4.7e-37	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t		score	E-value	—
7tm_1	1/1	57	321	1	259	[ ]	119.9	4.7e-37	

Alignments of top-scoring domains:

7tm_1: domain 1 of 1, from 57 to 321: score 119.9, E = 4.7e-37

```
              *->GNiLVilvilrtkklrtptnifilNLAVADLLflltlppwalyylvg
                 GN+ ++++++r +++r +t +++lNL  ADLLf  + p++ ++  -+
   Flh14273,  57  GNVCALVLVAR-RRRRGATACLVLNLFCADLLFISAIPLVLAVR-WT 101

              gaadWpfGsalCklvtaldvvnmyaSillLtalSiDRYlAlvhPlryrrr
              e.W++G++ C+l+ +++++++ +  il+L+a S++R + Iv  l+   +r
   Flh14373,102 --EAWLLGPVACHLLFYYMTLSGSVTILTLAAVSLERMVCIV-HLQRGVR 148

              rtsprrAkvvilvwvlalllslPpllfswvktveegngtlnvnvevCli
              +r +v+++l+W +++++lP +f+ v+  ++ ++ ++ +C++
   Flh14273,149 GPGRRARAVLLALIWGYSAVAALPLCVFFRVVPQRLPG--ADQEISICTL 196

              dfpccstasvstwlrsyvllstlwgFllPllvilvcYtrIlrtlr.....
              +p++++    ++s+ +++ ++ Fl+P lvi++ Y+ Il + + ++++
   Flh14273,197 IWPTIPG------EISWDVSFVTLNFLVPGLVIVISYSKILQITKasrkr 240

              ..................kaaktllvvvvvFvlCWlPyfivllldtlc
              + +  +++++ + ++++ ++ +tl++++v F++ W P  i++ll  +
   Flh14273,241 lcvslayseehqirvsqqdfRLFRTLFLLMVSFFIMWSPIIITILLILIQ 290

              .lsiimsstCelervlptallvtlwLayvNsclNPilY<-*
              -+         +  + p ++++ + ++++Na+lNPi+Y
   Flh14273,291 nFK-------QDLVIWPSLFFWVVAPTFANSALNPILY 321
```
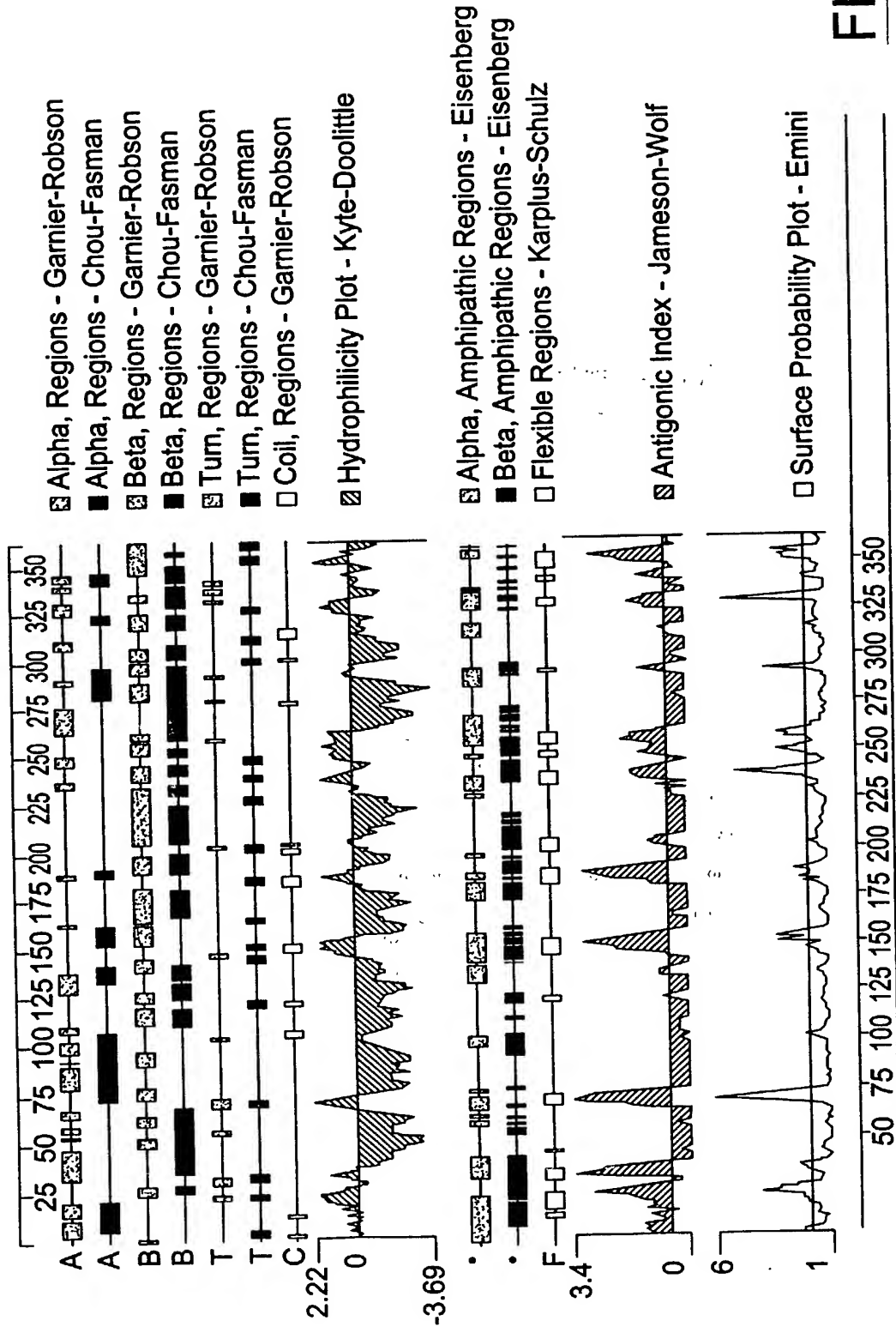
FIG. 2.

FIG. 3.

Analysis of Flh14273, (362 aa)

>Flh14273, 1086 bases, 1825 checksum.
MSPECARAAQDAPLRSLEQANRTRFPFFSDVKGDHRLVLAAVETTVLVLEFAVSLLGNVC
ALVLVARRRRRGATAQLVLNLFCADLLFYSAIPLVLAVRWTEAVLLGPVACHLLFYVMTL
SGSVTILTLAAVSLERMVCIVHLQRCVRGPGRRARAVLLALIWGYSAVAALPLCVFFRVV
PQRLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVISYSKILQITKASRKR
LTVSLAYSESHQIRVSQQDFRLFRTLFLLMVSFFIMWSPIIITILLILIQNFKQDLVIWP
SLFFWVVAFTFANSALNPILYNMTLCRNEWKKIFCCFWFGPEKGAILTDTSVKRNDLSIIS
G+

FIG. 4.

Prosite Pattern Matches for F1h14273

>PS00001/PD0C00001/ASN_GLYCOSYLATION N-glycosylation site.

Query: 21   NRTR 24
Query: 322   NMTL 325

>PS00004/PD0C00004/CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylatic

Query: 239   KRLT 242

>PS00005/PD0C00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 237   SRK   239
Query: 350   SVK   352

>PS00006/PD0C00006/CK2_PHOSPHO_SITE Casien kinase II phosphorylation site.

Query: 256   SQQD 259

>PS00008/PD0C00008/MYRISTYL N-myristoylation site.

Query: 57   GNVCAL 62
Query: 72   GATACL 77
Query: 343   GAILTD 348

>PS00009/PD0C00009/AMIDATION Amidation site.

Query: 150   PCRR 153

>PS00029/PD0C00029/LEUCINE_ZIPPER Leucine zipper pattern.

Query: 106   LGPVACHLLFYVMTLSGSVTIL   127

FIG. 5.

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
75	98	ins->out	4.0
113	134	out->ins	4.0
156	177	ins->out	4.9
209	227	out->ins	3.7
266	289	ins->out	6.5
297	321	out->ins	3.2

>F1h14273,
MSPECARAAGDAPLRSLEQANRTRFPFFSDVKGDHRLVLAAVETTVLVLIPAVSLLGNVC
ALVLVARRRRGATACLVLNLFCADLLFISAWPLVLAVRWTEAWLLGPVACHLLFYVMTL
SGSVTILTLAAVSLERMVCIVHLQRGVRGPGRRARAVLLALIWGYSAVAALPLCVFFRVV
PQRLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVISYSKILQITKASRKR
LTVSLAYSESHQIRVSQQDFRLFRTLFLLMVSFFIMWSPIIITILLILIQNFKQDLVIWP
SLFFWVVAFTFANSALNPILYNMTLCRNEWKKIFCCFWFPEKGAILTDTSVKRNDLSIIS
G

Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
14	37	ins->out	4.0
52	73	out->ins	4.0
95	116	ins->out	4.9
148	166	out->ins	3.7
205	228	ins->out	6.5
236	260	out->ins	3.2

>F1h14273,_mature
LVLVARRRRGATACLVLNLFCADLLFISAIPLVLAVRWTEAWLLGPVACHLLPYVMTLS
GSVTILTLAAVSLERMVCIVHLQRGVRGPGRRARAVLLALIWGYSAVAALPLCVFFRVVP
QRLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVISYSKILQITKASRKRL
TVSLAYSESHQIRVSQQDFRLFRTLFLLMVSFFIMWSPIIITILLILIQNFKQDLVIWPS
LFFWVVAFTFANSALNPILYNMTLCRNEWKKIPCCFWFPEKGAILTDTSVKRNDLSIISG

FIG. 6.

```
Input file 14273m; Output File 14273mtra
Sequence length 1560

TTGCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAGAGGGGTTCATGGAGTGCTTCACACCATCAGTGACCA

CTCCAGACTTGTCCGGCTTTACCCGAATCTTCACAGAGCGGAGTCGATGACCCTCTTGACAGCAGCCAGAGCGCGGCAGCTC

                                     M   S   P   E   C   A   Q   T   T   G      10
CGCCATCTTCCCGGACGCGGTGGGCGGGCCCGGC  ATG TCC CCT GAG TGT GCA CAG ACG ACG GGC     30

 P   G   S   H   T   L   D   Q   V   N   R   T   H   F   P   F   F   S   D        30
CCT GCT CCC TCG CAC ACC CTG GAC CAA GTC AAT CGC ACC CAC TTC CCT TTC TTC TCG GAT  90

 V   K   G   D   H   R   L   V   L   S   V   E   T   T   V   L   G   L   I         50
GTC AAG GGC GAC CAC CGG TTG GTG TTG AGC GTC GAG ACC ACC GTT CTG GGA CTC ATC     150

 F   V   S   L   G   N   V   C   A   L   V   R   R   R                            70
TTT GTC GTC TCA CTG CTG GGC AAC GTG TGT GCT CTA GTG CTG GCG CGC CGT CGG CGC     210

 R   G   A   S   L   V   L   N   L   F   C   A   D   L   F   T   S                 90
CGT GGG GCG TCA GCC TCA AGC CTG GTG CTC GTG TTG CTC GCG GAT TTG CTC TTC ACC AGC 270

 A   I   P   L   V   L   F   V   R   W   T   E   A   W   L   G   P   V   V         110
GCC ATC CCT CTA GTG CTC GTC GTG GCC TGG GAG GCC TGG CTG TTG GGG CCC GTC GTC     330

 C   H   L   L   F   Y   V   M   T   M   S   S   V   T   I   L   T   L   A         130
TGC CAC CTG CTC TTC TAC GTG ATG ACA ATG AGC AGC GTC ACG ATC CTC ACA CTG GCC     390

 A   V   S   L   E   R   M   V   C   I   V   R   L   R   R   L   S   G   P         150
GCG GTC AGC CTG GAG CGC ATG GTG TGC ATC GTG CGG CTC CGG CGC TTG AGC GGC CCG     450

 G   R   R   T   Q   A   A   L   A   L   F   I   W   G   Y   S   A   A   A         170
GGG CGG CGG ACT CAG GCA GCG GCA CTG CTG CTC TTC ATA TGG GGT TAC TCG GCG GCC GCG 510
```

TO FIG. 7B.

FIG. 7A.

FROM FIG. 7A.

```
  L   P   L   Y   I   L   F   R   V   V   P   Q   R   L   P   G   G   D   Q   E
 CTG CCC CTC TAC ATC TTG TTC CGC GTG GTC CCG CAG CGC CTT CCC GGC GGG GAC CAG GAA    190
                                                                                    627

  I   P   I   C   T   L   D   W   P   N   R   I   G   E   I   S   W   D   V   F
 ATT CCG ATT TGC ACA TTG GAT TGG CCC AAC CGC ATA GGA GAA ATC TCA TGG GAT GTG TTT    210
                                                                                    630

  F   E   T   L   N   F   L   V   P   G   L   V   I   S   Y   I   S   K   I
 TTT GAG ACT TTG AAC TTC CTG GTG CCG GGA CTG GTC ATT AGT TAC ATC TCC AAA ATT        230
                                                                                    690

  L   Q   I   T   K   A   S   R   K   R   L   T   L   S   A   Y   S   E   S
 TTA CAG ATC ACG AAA GCA TCG AGG AAG AGG CTT ACG CTC AGC GCA TAC TCT GAG AGC        250
                                                                                    750

  H   Q   I   R   V   S   Q   Q   D   Y   R   L   F   R   T   L   L   I   L   Q
 CAC CAG ATC CGA GTG TCC CAA CAA GAC TAC CGA CTC TTC CGC ACC ATC CTC ATC TTG CAA    270
                                                                                    810

  V   S   F   I   M   W   S   P   I   I   T   I   F   F   W   V   A   F   T
 GTT TCC TTC ATC ATG TGG AGT CCC ATC ATC ACC ATC TTC TTC TGG GTG GCC TTC ACG        290
                                                                                    870

  N   F   R   Q   D   L   V   I   W   P   S   L   Y   N   M   S   F   R   N   E   W
 AAC TTC CGG CAG GAC CTG GTC ATC TGG CCA TCC CTT TAC AAC ATG TCG TTC AGG AAC GAA TGG 310
                                                                                    930

  F   A   N   S   A   D   L   V   I   P   N   L   Y   N   S   L   F   R   N   E   W
 TTT GCC AAC TCT GCC CTA AAC CCC ATC AAC ATG TCG TTC AGG AAC GAA TGG                330
                                                                                    990

  R   K   I   F   C   F   F   P   E   K   G   A   I   F   T   D   T   S
 AGG AAG ATT TTT TGC TTC TTT CCA GAG AAG GGA GCC ATT TTT ACA GAT ACG TCT            350
                                                                                   1050

  V   R   R   N   D   L   S   V   I   S   S   *
 GTC AGG CGA AAT GAC TTG TCT GTT ATT TCC AGC TAA                                     362
                                                                                   1086
```

CTAGCCTCTGGTGCCAGGTGAACCACGGTGTGCATGTAAAGCGAGTTAACTTCAAGGAAAGCCACCAGTGCGCCCTGC
TTTAAAAATACCCGACTTCCAACAGCAGGCATCGTACGGAGCCAGCAAATTAAGGAATGATCGCTCAGTATAAAAATATT
TTTCCTTAAAGAACTTTCTATGGGTTCCTTTGTGAACTTTTTTAAGTGTGTTTGTAATGATCTAGTCAGTTAATAAATT
TTTATTTATAACGTGTTCCTACAAAAAAAAAAAAAAAAAAA

FIG. 7B.

Query: 14273m,

Scores for sequence family classification (score includes all domains):

Sequence	Description		Score	E-value	N
7tm_1	PF00001	7 transmembrane receptor (rhodopsin	118.8	1e-35	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t		score	E-value	—
7tm_1	1/1	57	321	..	1	259 [ ]	118.8	1e-36	

Alignments of top-scoring domains:
7tm_1: domain 1 of 1, from 57 to 321: score 118.8, E = 1e-36

```
                *->GNlLVilvilrtkklrtptnifilNLAvADLLfllt1ppwalyylvg
                   GN+ ++++++r +++r ++ +++1NL  ADLLf+ + p++ ++  ++
     14273m,  57   GNVCALVLVAR-RRRRGASASLVLNLFCADLLFTSAIPLVLVVR-WT 101


              gaadWpfGaalCklvtaldvvnmyaSill1Ltal SiDRYlAlvhPlryrrr
                e W++G+++C+l+ +++++++ +  il+L+a S++R + Iv  1r   +
     14273m,102 --EAWLLGPVVCHLLPYVMTMSGSVTILTLAAVSLERMVCIV-RLRRGLS 148


              rtsprrA.kvvillvWvlallls1Pp1lfswvktveagngtlnvnvtvCl
                 rr++++++++++W  ++1++1P ++++ v +    ++g    ++ +C+
     14273m,149 GP-GRRTqAALLAFIWGYSALAALPLYILFRVVPQRLPGGD--QEITPCT 195


              idfpeestasvstwlrsyvllstlvgF2lPllvilvoYtrllrtlr....
               +d+p++ +       ++s+ +++ ++ F1+P lvi++ Y+ 11 + + +++
     14273m,196 LDWPNRIG------EISWDVFFETLNFLVPGLVIVISYSKILQITKasrk 239


              ..................:.....kaaktllvvvvvFvlCWlPyfivllldt-
                + + +    +++++ + ++++ ++ +t1++++v F++ W P i++11  +
     14273m,240 rltlslayseshqirvsqqdyRLFRTLFLLMVSFFIMWSPIIITILLILI 289


              c.laiimestCelervlptallvtlwLayvNsclNPilY<-*
               ++          + + p ++++ + ++++Ns+1NPi+Y
     14273m,290 QnFR-------QDLVIWPSLFFWVVAFTFANSALNPILY 321
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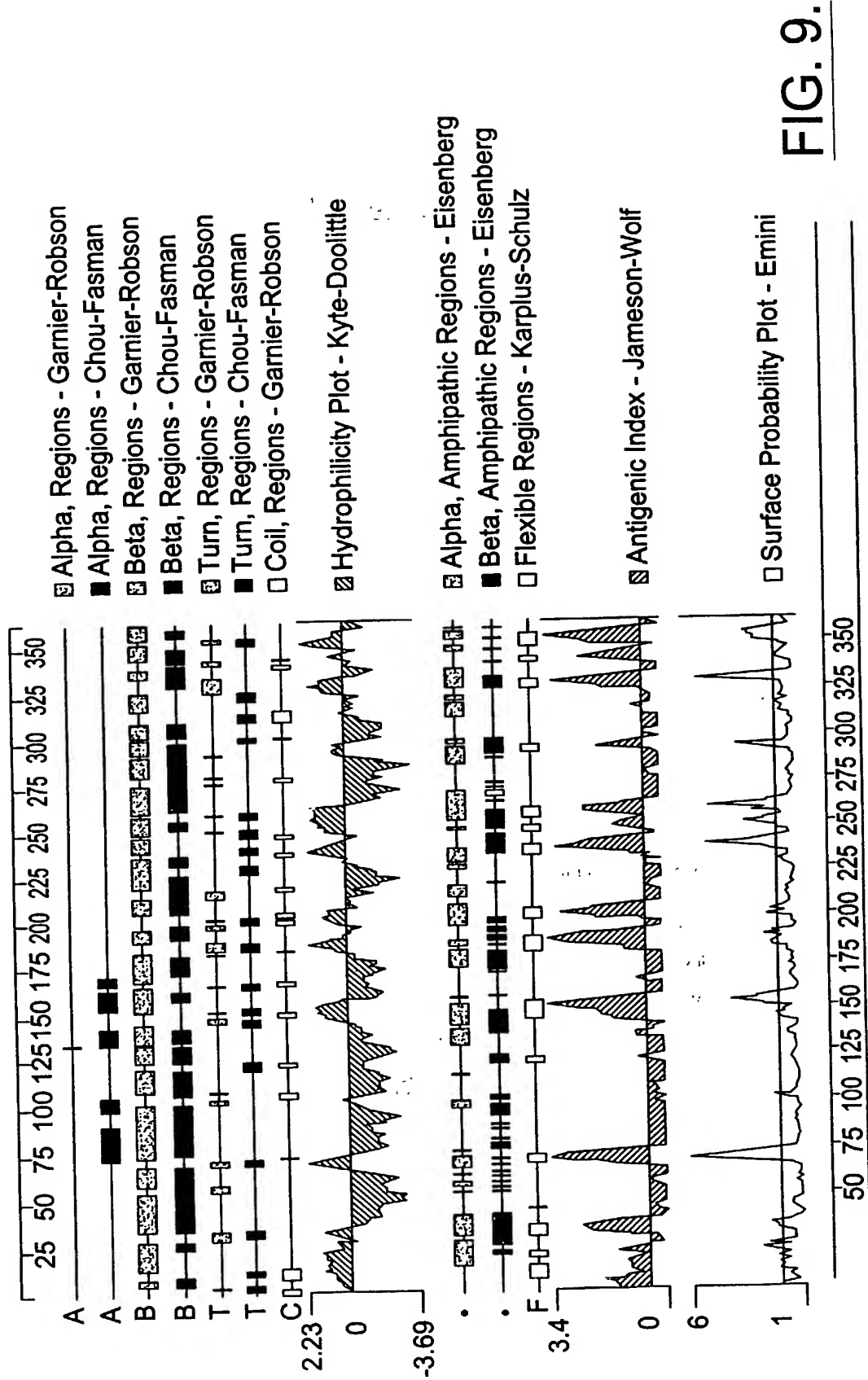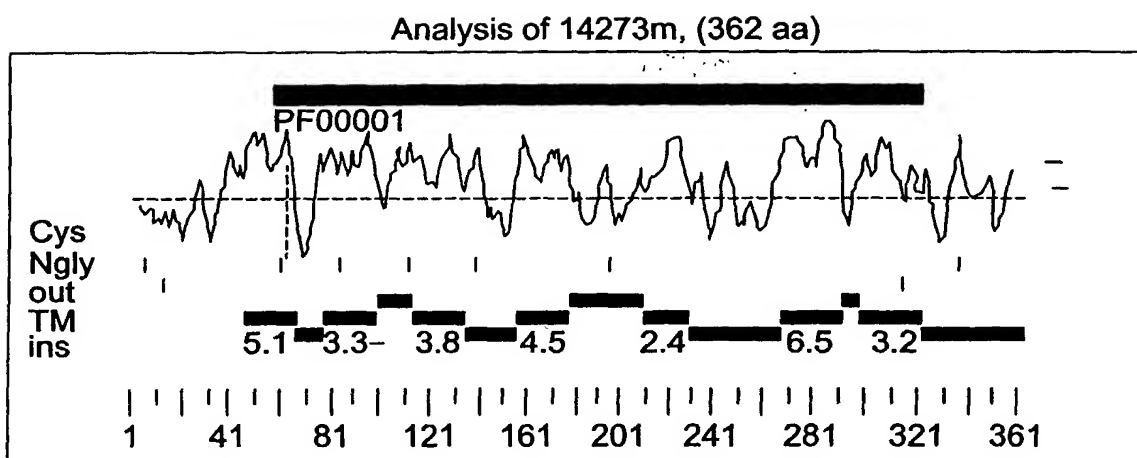
FIG. 8.

FIG. 9.

Analysis of 14273m, (362 aa)

>14273m, 1086 bases, 6943 checksum.
MSPECAQTTGPCPSHTLDQVNRTHFPFFSDVKGDHRLVLSVVETTVLGLIFVVSLLGNVC
ALVLVARRRRRGASASLVLNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFVVMTM
SGSVTILTLAAVSLERMVCIVRLRRGLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV
PQRLPGGDQEIPICTLDWPNRIGEISWDVFFETLNFLVPGLVIVISYSKILQITKASRKR
LTLSLAYSESHQIRVSQQDYRLFRTLFLLMVSFFIMWSPIIITILLILIQNFRQDLVIWP
SLFFWVVAFTFANSALNPILYNMSLFRNEWRKIFCCFPFPEKGAIFTDTSVRRNDLSVIS
S*

FIG. 10.

Prosite Pattern Matches for 14273m,

>PS00001/PD0C00001;ASN_GLYCOSYLATION N-glycosylation site.

Query: 21   NRTH   24
Query: 322   NRTH   325

>PS00002/PD0C00002/GLYCOSAMINOGLYCAN Glycosaminoglycan attachment site.
          RU   Additional rules:
          RU   There must be at least two acidic amino acids (Glu or Asp) from -2 to
                  -4 relative to the serine.
Query: 148   SGPG   151

>PS00004/PD0C00004/CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation

Query: 239   KRLT   242

>PS00005/PD0C00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 237   SRK   239
Query: 350   SVR   352

>PS00006/PD0C00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 40   SVVE   43
Query: 256   SQQD   259

>PS00008/PD0C00008/MYRISTYL N-myristoylation site.

Query: 57   GNVCAL   62
Query: 72   GASASL   77
Query: 343   GAIFTD   348

>PS00009/PD0C00009/AMIDATION Amidation site.

Query: 150   PGRR   153

FIG. 11.

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
77	98	ins->out	3.3
113	134	out->ins	3.8
156	177	ins->out	4.5
209	227	out->ins	2.4
266	289	ins->out	6.5
297	321	out->ins	3.2

>14273m,
MSPECAQTTGPGPSHTLDQVNRTHFPFFSDVKGDHRLVLSVVETTVLGLIFVVSLLGNVC
ALVLVARRRRGASASLVLNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMTM
SGSVTILTLAAVSLERMVCIVRLRRGLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV
PQRLPGGDQEIPICTLDWPNRIGEISWDVFFETLNFLVPGLVIVISYSKILQITKASRKR
LTLSLAYSESHQIRVSQQDYRLFRTLFLLMVSFFIMWSPIIIITILLILIQNFRQDLVIWP
SLFFWVVAFTFANSALNPILYMMSLFRNEWRKIFCCFFFPEKGAIFTDTSVRRNDLSVIS
S

Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
16	37	ins->out	3.3
52	73	out->ins	3.8
95	116	ins->out	4.5
148	166	out->ins	2.4
205	228	ins->out	6.5
236	260	out->ins	3.2

>14273m, _mature
LVLVARRRRGASASLVLNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMGMS
GSVTILTLAAVSLERMVCIVRLRRGLSGPGRRTQAAIIAFIWGYSALAALPLYILFRVVP
QRLPGGDQEIPICTLDWPNRIGEISWCVFFETLNFLVPGLVIVISYSKILQITKASRKRL
TLSLAYSESKQIRVSQQDYRLFRTLFLLMVSFFTMWSPIIIITILLILIQNFRQDLVIWPS
LFFWVVAFTFANSALNPILYNMSLFRNEWRKIFCCFFFPEKGAIFTDTSVRRNDLSVISS

FIG. 12.